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Q fever is a zoonotic disease caused by the intracellular bacterium *Coxiella burnetii*. Humans become infected mainly through inhalation of contaminated aerosols generated by birth products, as well as various other excreta shed by infected cattle, sheep and goats. Starting in 2007, the Netherlands experienced the largest outbreak of Q fever ever reported in literature and it was linked to episodes of abortion in large dairy goat farms. The dimensions of goat and sheep farms in Switzerland differ substantially from those in the Netherlands. However, the likelihood for a larger outbreak of Q fever in Switzerland is not known. The aim of this project was to study the seroprevalence of Q fever in sheep and goats and to assess the risk for a larger outbreak in humans. Prevalence was determined from a representative sample of 72 goat farms and 100 sheep farms respectively. Samples collected for the 2011 nationwide cross-sectional survey to document freedom from *Brucella melitensis* were analyzed by ELISA. Herd level prevalence ranged from 5% in sheep to 11.1% in goat flocks. At animal level, prevalence was 1.8% in sheep and 3.4% in goats, respectively. In addition, we quantified the bacteria in aborted material using PCR, in order to obtain information on the extent of environmental contamination following abortions. Furthermore, these samples will be used to identify virulence factors, as well as the genotypes present in Switzerland. A literature search on Q fever epidemiology was used to identify risk pathways and to generate a qualitative risk assessment for human infection. Finally a sensitivity analysis will reveal which factors have the greatest influence on the probability of larger outbreaks of Q fever in humans. These results form an important basis for future prevention- and control strategies for Q fever.